METHODS FOR IDENTIFYING DRUG TARGETS
BASED ON GENOMIC SEQUENCE DATA

Abstract of the Disclosure

This invention provides a computational approach to identifying potential antibacterial drug targets based on a genome sequence and its annotation. Starting from a fully sequenced genome, open reading frame assignments are made which determine the metabolic genotype for the organism. The metabolic genotype, and more specifically its stoichiometric matrix, are analyzed using flux balance analysis to assess the effects of genetic deletions on the fitness of the organism and its ability to produce essential biomolecules required for growth.